

Amendments to the Specification:

Please delete the current Abstract and replace it with the revised Abstract contained on a single sheet attached hereto.

Before the paragraph starting on page 9, line 2, please add the following new paragraphs:

According to one aspect of the invention, there is disclosed a method for the multidimensional analysis of a proteome in which the biological material with the proteome to be analyzed is solubilized and the proteins belonging to the proteome are separated, quantitatively determined and identified. The first step is subjecting the proteome to a number n of different separating processes for $n > 2$ under standardized conditions in such a way that each of the liquid fractions m_1 obtained in a separating step supplies m_2 liquid fractions in a subsequent separating step, wherein, after n separating steps, there are $m_1 * m_2 * \dots * m_n = M$ liquid fractions. The second step is identifying said $m_1 * m_2 * \dots * m_n = M$ liquid fractions by τ different analysis processes qualitatively and/or quantitatively by identification processes, and determining said liquid fractions quantitatively by known quantification processes. After combining the analysis data, the third step is obtaining an n -dimensional image of the proteome which is characterized by identifiers and quantifiers and by the position in the n -dimensional data space.

According to another aspect of the invention, one or more of the following methods are selected as separating methods: methods which separate according to the size of the protein; and/or methods which separate according to the mass of the protein; and/or methods which separate according to the charge of the protein; and/or methods which separate according to the hydrophobicity of the protein; methods which separate according to the shape of the protein; and/or methods which separate according to the affinity of the protein, with respect to specific ligands, also to antibodies.

According to another aspect of the invention, methods for determining specific immunological characteristics and/or methods for determining specific catalytic activity

and/or methods for determining chemical modification of the proteins of the proteome are used as identification methods.

According to another aspect of the invention, methods for nonspecific determination of protein concentration with different sensitivities and/or quantitative determination methods for determining specific catalytic activities and/or quantitative immunological methods and/or quantitative binding assays are selected as the quantification processes.

According to another aspect of the invention, the identification of individual proteins of the proteome is carried out directly by mass determination of the proteins.

According to another aspect of the invention, the identification of individual proteins is carried out according to protease digestion and mass identification of fragments.

According to another aspect of the invention, after at least one separation step, the fractions are assembled in a two-dimensional multiple vessel system, with the layout of microtitration plates.

According to another aspect of the invention, in the first separating step, the fractions are assembled in a defined grid, preferably in the n * 96 grid of microtitration technology.

According to another aspect of the invention, all identification and quantification steps are carried out in a defined grid, preferably in the n * 96 grid, with adaptable liquid handling technique.

According to another aspect of the invention, all identification steps and quantification steps are carried out with at least four two-dimensionally arranged, simultaneously working pipettor channels.

According to another aspect of the invention, the first dimension for separation is high-resolution size exclusion, ion exchange or hydrophobicity chromatography, in that the second dimension is carried out by parallel separation and fractionation of the fractions of the first dimension by a principle of separation other than that used for the first dimension, and in that each further separation and fractionation is carried out by parallel separating and fractionating methods with the fractions obtained from the preceding separating and fractionating steps.

According to another aspect of the invention, the analysis data for the n-dimensional image of the protein are assembled in a database, said analysis data being

associated with said M liquid fractions.